



1/17

SEQUENCE LISTING

<110> HSC Research and Development Limited Partnership

<120> Human Lymphoid Protein Tyrosine Phosphatases

<130> 92906-2

10 <140> US 09/600358

<141> 2000-09-25

<150> CA 2,220,853

<151> 1998-01-16

<160> 7

<170> PatentIn Ver. 2.0

20

<210> 1

<211> 3058

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (42)..(2465)

30 <400> 1

tccctcaacc tacttataga ctatctttct tgctctgcag c atg gac caa aga gaa 56  
Met Asp Gln Arg Glu  
1 5

att ctg cag aag ttc ctg gat gag gcc caa agc aag aaa att act aaa 104  
Ile Leu Gln Lys Phe Leu Asp Glu Ala Gln Ser Lys Lys Ile Thr Lys  
10 15 20

40 gag gag ttt gcc aat gaa ttt ctg aag ctg aaa agg caa tct acc aag 152  
Glu Glu Phe Ala Asn Glu Phe Leu Lys Leu Lys Arg Gln Ser Thr Lys  
25 30 35

tac aag gca gac aaa acc tat cct aca act gtg gct gag aat gcc aag 200  
Tyr Lys Ala Asp Lys Thr Tyr Pro Thr Thr Val Ala Glu Asn Ala Lys  
40 45 50

aat atc aag aaa aac aga tat aag gat att ttg ccc tat gat tat agc 248  
Asn Ile Lys Lys Asn Arg Tyr Lys Asp Ile Leu Pro Tyr Asp Tyr Ser  
55 60 65

50

cgg gta gaa cta tcc ctg ata acc tct gat gag gat tcc agc tac atc 296  
Arg Val Glu Leu Ser Leu Ile Thr Ser Asp Glu Asp Ser Ser Tyr Ile  
70 75 80 85

aat gcc aac ttc att aag gga gtt tat gga ccc aag gct tat att gcc 344  
Asn Ala Asn Phe Ile Lys Gly Val Tyr Gly Pro Lys Ala Tyr Ile Ala  
90 95 100

RECEIVED

MAY 15 2002

TECH CENTER 1600/2900

	acc cag ggt cct tta tct aca acc ctc ctg gac ttc tgg agg atg att	392
	Thr Gln Gly Pro Leu Ser Thr Thr Leu Leu Asp Phe Trp Arg Met Ile	
	105 110 115	
	tgg gaa tat agt gtc ctt atc att gtt atg gca tgc atg gag tat gaa	440
	Trp Glu Tyr Ser Val Leu Ile Ile Val Met Ala Cys Met Glu Tyr Glu	
	120 125 130	
10	atg gga aag aaa aag tgt gag cgc tac tgg gct gag cca gga gag atg	488
	Met Gly Lys Lys Lys Cys Glu Arg Tyr Trp Ala Glu Pro Gly Glu Met	
	135 140 145	
	cag ctg gaa ttt ggc cct ttc tct gta tcc tgt gaa gct gaa aaa agg	536
	Gln Leu Glu Phe Gly Pro Phe Ser Val Ser Cys Glu Ala Glu Lys Arg	
	150 155 160 165	
	aaa tct gat tat ata atc agg act cta aaa gtt aag ttc aat agt gaa	584
	Lys Ser Asp Tyr Ile Ile Arg Thr Leu Lys Val Lys Phe Asn Ser Glu	
	170 175 180	
20	act cga act atc tac cag ttt cat tac aag aat tgg cca gac cat gat	632
	Thr Arg Thr Ile Tyr Gln Phe His Tyr Lys Asn Trp Pro Asp His Asp	
	185 190 195	
	gta cct tca tct ata gac cct att ctt gag ctc atc tgg gat gta cgt	680
	Val Pro Ser Ser Ile Asp Pro Ile Leu Glu Leu Ile Trp Asp Val Arg	
	200 205 210	
	tgt tac caa gag gat gac agt gtt ccc ata tgc att cac tgc agt gct	728
30	Cys Tyr Gln Glu Asp Asp Ser Val Pro Ile Cys Ile His Cys Ser Ala	
	215 220 225	
	ggc tgt gga agg act ggt gtt att tgt gct att gtt gat tat aca tgg	776
	Gly Cys Gly Arg Thr Gly Val Ile Cys Ala Ile Val Asp Tyr Thr Trp	
	230 235 240 245	
	atg ttg cta aaa gat ggg ata att cct gag aac ttc agt gtt ttc agt	824
	Met Leu Leu Lys Asp Gly Ile Ile Pro Glu Asn Phe Ser Val Phe Ser	
	250 255 260	
40	ttg atc cgg gaa atg cgg aca cag agg cct tca tta gtt caa acg cag	872
	Leu Ile Arg Glu Met Arg Thr Gln Arg Pro Ser Leu Val Gln Thr Gln	
	265 270 275	
	gaa caa tat gaa ctg gtc tac aat gct gta tta gaa cta ttt aag aga	920
	Glu Gln Tyr Glu Leu Val Tyr Asn Ala Val Leu Glu Leu Phe Lys Arg	
	280 285 290	
	cag atg gat gtt atc aga gat aaa cat tct gga aca gag agt caa gca	968
50	Gln Met Asp Val Ile Arg Asp Lys His Ser Gly Thr Glu Ser Gln Ala	
	295 300 305	
	aag cat tgt att cct gag aaa aat cac act ctc caa gca gac tct tat	1016
	Lys His Cys Ile Pro Glu Lys Asn His Thr Leu Gln Ala Asp Ser Tyr	
	310 315 320 325	

	tct cct aat tta cca aaa agt acc aca aaa gca gca aaa atg atg aac	1064
	Ser Pro Asn Leu Pro Lys Ser Thr Thr Lys Ala Ala Lys Met Met Asn	
	330 335 340	
	caa caa agg aca aaa atg gaa atc aaa gaa tct tct tcc ttt gac ttt	1112
	Gln Gln Arg Thr Lys Met Glu Ile Lys Glu Ser Ser Ser Phe Asp Phe	
	345 350 355	
10	agg act tct gaa ata agt gca aaa gaa gag cta gtt ttg cac cct gct	1160
	Arg Thr Ser Glu Ile Ser Ala Lys Glu Glu Leu Val Leu His Pro Ala	
	360 365 370	
	aaa tca agc act tct ttt gac ttt ctg gag cta aat tac agt ttt gac	1208
	Lys Ser Ser Thr Ser Phe Asp Phe Leu Glu Leu Asn Tyr Ser Phe Asp	
	375 380 385	
20	aaa aat gct gac aca acc atg aaa tgg cag aca aag gca ttt cca ata	1256
	Lys Asn Ala Asp Thr Thr Met Lys Trp Gln Thr Lys Ala Phe Pro Ile	
	390 395 400 405	
	gtt ggg gag cct ctt cag aag cat caa agt ttg gat ttg ggc tct ctt	1304
	Val Gly Glu Pro Leu Gln Lys His Gln Ser Leu Asp Leu Gly Ser Leu	
	410 415 420	
	ttg ttt gag gga tgt tct aat tct aaa cct gta aat gca gca gga aga	1352
	Leu Phe Glu Gly Cys Ser Asn Ser Lys Pro Val Asn Ala Ala Gly Arg	
	425 430 435	
30	tat ttt aat tca aag gtg cca ata aca cgg acc aaa tca act cct ttt	1400
	Tyr Phe Asn Ser Lys Val Pro Ile Thr Arg Thr Lys Ser Thr Pro Phe	
	440 445 450	
	gaa ttg ata cag cag aga gaa acc aag gag gtg gac agc aag gaa aac	1448
	Glu Leu Ile Gln Gln Arg Glu Thr Lys Glu Val Asp Ser Lys Glu Asn	
	455 460 465	
40	ttt tct tat ttg gaa tct caa cca cat gat tct tgt ttt gta gag atg	1496
	Phe Ser Tyr Leu Glu Ser Gln Pro His Asp Ser Cys Phe Val Glu Met	
	470 475 480 485	
	cag gct caa aaa gta atg cat gtt tct tca gca gaa ctg aat tat tca	1544
	Gln Ala Gln Lys Val Met His Val Ser Ser Ala Glu Leu Asn Tyr Ser	
	490 495 500	
	ctg cca tat gac tct aaa cac caa ata cgt aat gcc tct aat gta aag	1592
	Leu Pro Tyr Asp Ser Lys His Gln Ile Arg Asn Ala Ser Asn Val Lys	
	505 510 515	
50	cac cat gac tct agt gct ctt ggt gta tat tct tac ata cct tta gtg	1640
	His His Asp Ser Ser Ala Leu Gly Val Tyr Ser Tyr Ile Pro Leu Val	
	520 525 530	
	gaa aat cct tat ttt tca tca tgg cct cca agt ggt acc agt tct aag	1688
	Glu Asn Pro Tyr Phe Ser Ser Trp Pro Pro Ser Gly Thr Ser Ser Lys	
	535 540 545	

	atg tct ctt gat tta cct gag aag caa gat gga act gtt ttt cct tct	1736
	Met Ser Leu Asp Leu Pro Glu Lys Gln Asp Gly Thr Val Phe Pro Ser	
	550 555 560 565	
	tct ctg ttg cca aca tcc tct aca tcc ctc ttc tct tat tac aat tca	1784
	Ser Leu Leu Pro Thr Ser Ser Thr Ser Leu Phe Ser Tyr Tyr Asn Ser	
	570 575 580	
10	cat agt tct tta tca ctg aat tct cca acc aat att tcc tca cta ttg	1832
	His Ser Ser Leu Ser Leu Asn Ser Pro Thr Asn Ile Ser Ser Leu Leu	
	585 590 595	
	aac cag gag tca gct gta cta gca act gct cca agg ata gat gat gaa	1880
	Asn Gln Glu Ser Ala Val Leu Ala Thr Ala Pro Arg Ile Asp Asp Glu	
	600 605 610	
	atc ccc cct cca ctt cct gta cgg aca cct gaa tca ttt att gtg gtt	1928
	Ile Pro Pro Pro Leu Pro Val Arg Thr Pro Glu Ser Phe Ile Val Val	
	615 620 625	
20	gag gaa gct gga gaa ttc tca cca aat gtt ccc aaa tcc tta tcc tca	1976
	Glu Glu Ala Gly Glu Phe Ser Pro Asn Val Pro Lys Ser Leu Ser Ser	
	630 635 640 645	
	gct gtg aag gta aaa att gga aca tca ctg gaa tgg ggt gga aca tct	2024
	Ala Val Lys Val Lys Ile Gly Thr Ser Leu Glu Trp Gly Gly Thr Ser	
	650 655 660	
30	gaa cca aag aaa ttt gat gac tct gtg ata ctt aga cca agc aag agt	2072
	Glu Pro Lys Lys Phe Asp Asp Ser Val Ile Leu Arg Pro Ser Lys Ser	
	665 670 675	
	gta aaa ctc cga agt cct aaa tca gaa cta cat caa gat cgt tct tct	2120
	Val Lys Leu Arg Ser Pro Lys Ser Glu Leu His Gln Asp Arg Ser Ser	
	680 685 690	
	ccc cca cct cct ctc cca gaa aga act cta gag tcc ttc ttt ctt gcc	2168
	Pro Pro Pro Pro Leu Pro Glu Arg Thr Leu Glu Ser Phe Phe Leu Ala	
	695 700 705	
40	gat gaa gat tgt atg cag gcc caa tct ata gaa aca tat tct act agc	2216
	Asp Glu Asp Cys Met Gln Ala Gln Ser Ile Glu Thr Tyr Ser Thr Ser	
	710 715 720 725	
	tat cct gac acc atg gaa aat tca aca tct tca aaa cag aca ctg aag	2264
	Tyr Pro Asp Thr Met Glu Asn Ser Thr Ser Ser Lys Gln Thr Leu Lys	
	730 735 740	
50	act cct gga aaa agt ttc aca agg agt aag agt ttg aaa att ttg cga	2312
	Thr Pro Gly Lys Ser Phe Thr Arg Ser Lys Ser Leu Lys Ile Leu Arg	
	745 750 755	
	aac atg aaa aag agt atc tgt aat tct tgc cca cca aac aag cct gca	2360
	Asn Met Lys Lys Ser Ile Cys Asn Ser Cys Pro Pro Asn Lys Pro Ala	
	760 765 770	

gaa tct gtt cag tca aat aac tcc agc tca ttt ctg aat ttt ggt ttt 2408  
 Glu Ser Val Gln Ser Asn Asn Ser Ser Ser Phe Leu Asn Phe Gly Phe  
 775 780 785

gca aac cgt ttt tca aaa ccc aaa gga cca agg aat cca cca cca act 2456  
 Ala Asn Arg Phe Ser Lys Pro Lys Gly Pro Arg Asn Pro Pro Pro Thr  
 790 795 800 805

10 tgg aat att taataaaact cagatttata ataatatggg ctgcaagtac 2505  
 Trp Asn Ile

acctgcaaat aaaactacta gaatactgct agttaaaata agtgctctat atgcataata 2565  
 tgaagatatg ctaatgtgtt aatagctttt aaaagaaaag caaaatgccca ataagtgccca 2625  
 gttttgcatt ttcatatcat ttgcattgag ttgaaaactg caaataaaaag tttgtcactt 2685  
 gagcttatgt acagaatgct atatgagaaa cactttttaga atggatttat ttttcatttt 2745  
 tgccagttat ttttattttc ttttactttt ctacataaac ataaacttca aaaggtttgt 2805  
 aagatttggga tctcaactaa tttctacatt gccagaatat actataaaaa gttaaaaaaa 2865  
 aaaacttact ttgtgggttg caatacaaac tgctcttgac aatgactatt ccctgacagt 2925  
 tatttttgcc taaatggagt ataccttgta aatcttccca aatgttgttg aaaactggaa 2985  
 20 tattaagaaa atgagaaatt atatttatta gaataaaatg tgcaaataat gacaattatt 3045  
 tgaatgtaac aag 3058

<210> 2  
 <211> 808  
 <212> PRT  
 <213> Homo sapiens

<400> 2  
 30 Met Asp Gln Arg Glu Ile Leu Gln Lys Phe Leu Asp Glu Ala Gln Ser  
 1 5 10 15

Lys Lys Ile Thr Lys Glu Glu Phe Ala Asn Glu Phe Leu Lys Leu Lys  
 20 25 30

Arg Gln Ser Thr Lys Tyr Lys Ala Asp Lys Thr Tyr Pro Thr Thr Val  
 35 40 45

40 Ala Glu Asn Ala Lys Asn Ile Lys Lys Asn Arg Tyr Lys Asp Ile Leu  
 50 55 60

Pro Tyr Asp Tyr Ser Arg Val Glu Leu Ser Leu Ile Thr Ser Asp Glu  
 65 70 75 80

Asp Ser Ser Tyr Ile Asn Ala Asn Phe Ile Lys Gly Val Tyr Gly Pro  
 85 90 95

50 Lys Ala Tyr Ile Ala Thr Gln Gly Pro Leu Ser Thr Thr Leu Leu Asp  
 100 105 110

Phe Trp Arg Met Ile Trp Glu Tyr Ser Val Leu Ile Ile Val Met Ala  
 115 120 125

Cys Met Glu Tyr Glu Met Gly Lys Lys Lys Cys Glu Arg Tyr Trp Ala  
 130 135 140

Glu Pro Gly Glu Met Gln Leu Glu Phe Gly Pro Phe Ser Val Ser Cys  
 145 150 155 160

	Glu	Ala	Glu	Lys	Arg	Lys	Ser	Asp	Tyr	Ile	Ile	Arg	Thr	Leu	Lys	Val	
					165					170					175		
	Lys	Phe	Asn	Ser	Glu	Thr	Arg	Thr	Ile	Tyr	Gln	Phe	His	Tyr	Lys	Asn	
				180					185					190			
	Trp	Pro	Asp	His	Asp	Val	Pro	Ser	Ser	Ile	Asp	Pro	Ile	Leu	Glu	Leu	
			195					200					205				
10	Ile	Trp	Asp	Val	Arg	Cys	Tyr	Gln	Glu	Asp	Asp	Ser	Val	Pro	Ile	Cys	
		210					215					220					
	Ile	His	Cys	Ser	Ala	Gly	Cys	Gly	Arg	Thr	Gly	Val	Ile	Cys	Ala	Ile	
	225					230					235					240	
	Val	Asp	Tyr	Thr	Trp	Met	Leu	Leu	Lys	Asp	Gly	Ile	Ile	Pro	Glu	Asn	
					245					250					255		
20	Phe	Ser	Val	Phe	Ser	Leu	Ile	Arg	Glu	Met	Arg	Thr	Gln	Arg	Pro	Ser	
				260					265					270			
	Leu	Val	Gln	Thr	Gln	Glu	Gln	Tyr	Glu	Leu	Val	Tyr	Asn	Ala	Val	Leu	
			275					280					285				
	Glu	Leu	Phe	Lys	Arg	Gln	Met	Asp	Val	Ile	Arg	Asp	Lys	His	Ser	Gly	
	290						295					300					
	Thr	Glu	Ser	Gln	Ala	Lys	His	Cys	Ile	Pro	Glu	Lys	Asn	His	Thr	Leu	
	305					310					315					320	
30	Gln	Ala	Asp	Ser	Tyr	Ser	Pro	Asn	Leu	Pro	Lys	Ser	Thr	Thr	Lys	Ala	
					325					330					335		
	Ala	Lys	Met	Met	Asn	Gln	Gln	Arg	Thr	Lys	Met	Glu	Ile	Lys	Glu	Ser	
				340					345					350			
	Ser	Ser	Phe	Asp	Phe	Arg	Thr	Ser	Glu	Ile	Ser	Ala	Lys	Glu	Glu	Leu	
			355					360					365				
40	Val	Leu	His	Pro	Ala	Lys	Ser	Ser	Thr	Ser	Phe	Asp	Phe	Leu	Glu	Leu	
		370					375					380					
	Asn	Tyr	Ser	Phe	Asp	Lys	Asn	Ala	Asp	Thr	Thr	Met	Lys	Trp	Gln	Thr	
	385					390					395					400	
	Lys	Ala	Phe	Pro	Ile	Val	Gly	Glu	Pro	Leu	Gln	Lys	His	Gln	Ser	Leu	
					405					410					415		
	Asp	Leu	Gly	Ser	Leu	Leu	Phe	Glu	Gly	Cys	Ser	Asn	Ser	Lys	Pro	Val	
				420					425					430			
50	Asn	Ala	Ala	Gly	Arg	Tyr	Phe	Asn	Ser	Lys	Val	Pro	Ile	Thr	Arg	Thr	
			435					440					445				
	Lys	Ser	Thr	Pro	Phe	Glu	Leu	Ile	Gln	Gln	Arg	Glu	Thr	Lys	Glu	Val	
			450				455					460					

	Asp	Ser	Lys	Glu	Asn	Phe	Ser	Tyr	Leu	Glu	Ser	Gln	Pro	His	Asp	Ser	465	470	475	480
	Cys	Phe	Val	Glu	Met	Gln	Ala	Gln	Lys	Val	Met	His	Val	Ser	Ser	Ala	485	490	495	
	Glu	Leu	Asn	Tyr	Ser	Leu	Pro	Tyr	Asp	Ser	Lys	His	Gln	Ile	Arg	Asn	500	505	510	
10	Ala	Ser	Asn	Val	Lys	His	His	Asp	Ser	Ser	Ala	Leu	Gly	Val	Tyr	Ser	515	520	525	
	Tyr	Ile	Pro	Leu	Val	Glu	Asn	Pro	Tyr	Phe	Ser	Ser	Trp	Pro	Pro	Ser	530	535	540	
	Gly	Thr	Ser	Ser	Lys	Met	Ser	Leu	Asp	Leu	Pro	Glu	Lys	Gln	Asp	Gly	545	550	555	560
20	Thr	Val	Phe	Pro	Ser	Ser	Leu	Leu	Pro	Thr	Ser	Ser	Thr	Ser	Leu	Phe	565	570	575	
	Ser	Tyr	Tyr	Asn	Ser	His	Ser	Ser	Leu	Ser	Leu	Asn	Ser	Pro	Thr	Asn	580	585	590	
	Ile	Ser	Ser	Leu	Leu	Asn	Gln	Glu	Ser	Ala	Val	Leu	Ala	Thr	Ala	Pro	595	600	605	
30	Arg	Ile	Asp	Asp	Glu	Ile	Pro	Pro	Pro	Leu	Pro	Val	Arg	Thr	Pro	Glu	610	615	620	
	Ser	Phe	Ile	Val	Val	Glu	Glu	Ala	Gly	Glu	Phe	Ser	Pro	Asn	Val	Pro	625	630	635	640
	Lys	Ser	Leu	Ser	Ser	Ala	Val	Lys	Val	Lys	Ile	Gly	Thr	Ser	Leu	Glu	645	650	655	
	Trp	Gly	Gly	Thr	Ser	Glu	Pro	Lys	Lys	Phe	Asp	Asp	Ser	Val	Ile	Leu	660	665	670	
40	Arg	Pro	Ser	Lys	Ser	Val	Lys	Leu	Arg	Ser	Pro	Lys	Ser	Glu	Leu	His	675	680	685	
	Gln	Asp	Arg	Ser	Ser	Pro	Pro	Pro	Pro	Leu	Pro	Glu	Arg	Thr	Leu	Glu	690	695	700	
	Ser	Phe	Phe	Leu	Ala	Asp	Glu	Asp	Cys	Met	Gln	Ala	Gln	Ser	Ile	Glu	705	710	715	720
50	Thr	Tyr	Ser	Thr	Ser	Tyr	Pro	Asp	Thr	Met	Glu	Asn	Ser	Thr	Ser	Ser	725	730	735	
	Lys	Gln	Thr	Leu	Lys	Thr	Pro	Gly	Lys	Ser	Phe	Thr	Arg	Ser	Lys	Ser	740	745	750	
	Leu	Lys	Ile	Leu	Arg	Asn	Met	Lys	Lys	Ser	Ile	Cys	Asn	Ser	Cys	Pro	755	760	765	

Pro Asn Lys Pro Ala Glu Ser Val Gln Ser Asn Asn Ser Ser Ser Phe  
 770 775 780

Leu Asn Phe Gly Phe Ala Asn Arg Phe Ser Lys Pro Lys Gly Pro Arg  
 785 790 795 800

Asn Pro Pro Pro Thr Trp Asn Ile  
 805

10

<210> 3  
 <211> 2356  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (42)..(2117)

20

<400> 3  
 tccctcaacc tacttataga ctatttttct tgctctgcag c atg gac caa aga gaa 56  
 Met Asp Gln Arg Glu  
 1 5

att ctg cag aag ttc ctg gat gag gcc caa agc aag aaa att act aaa 104  
 Ile Leu Gln Lys Phe Leu Asp Glu Ala Gln Ser Lys Lys Ile Thr Lys  
 10 15 20

30

gag gag ttt gcc aat gaa ttt ctg aag ctg aaa agg caa tct acc aag 152  
 Glu Glu Phe Ala Asn Glu Phe Leu Lys Leu Lys Arg Gln Ser Thr Lys  
 25 30 35

tac aag gca gac aaa acc tat cct aca act gtg gct gag aat gcc aag 200  
 Tyr Lys Ala Asp Lys Thr Tyr Pro Thr Thr Val Ala Glu Asn Ala Lys  
 40 45 50

aat atc aag aaa aac aga tat aag gat att ttg ccc tat gat tat agc 248  
 Asn Ile Lys Lys Asn Arg Tyr Lys Asp Ile Leu Pro Tyr Asp Tyr Ser  
 55 60 65

40

cgg gta gaa cta tcc ctg ata acc tct gat gag gat tcc agc tac atc 296  
 Arg Val Glu Leu Ser Leu Ile Thr Ser Asp Glu Asp Ser Ser Tyr Ile  
 70 75 80 85

aat gcc aac ttc att aag gga gtt tat gga ccc aag gct tat att gcc 344  
 Asn Ala Asn Phe Ile Lys Gly Val Tyr Gly Pro Lys Ala Tyr Ile Ala  
 90 95 100

50

acc cag ggt cct tta tct aca acc ctc ctg gac ttc tgg agg atg att 392  
 Thr Gln Gly Pro Leu Ser Thr Thr Leu Leu Asp Phe Trp Arg Met Ile  
 105 110 115

tgg gaa tat agt gtc ctt atc att gtt atg gca tgc atg gag tat gaa 440  
 Trp Glu Tyr Ser Val Leu Ile Ile Val Met Ala Cys Met Glu Tyr Glu  
 120 125 130



	atg gga aag aaa aag tgt gag cgc tac tgg gct gag cca gga gag atg	488
	Met Gly Lys Lys Lys Cys Glu Arg Tyr Trp Ala Glu Pro Gly Glu Met	
	135 140 145	
	cag ctg gaa ttt ggc cct ttc tct gta tcc tgt gaa gct gaa aaa agg	536
	Gln Leu Glu Phe Gly Pro Phe Ser Val Ser Cys Glu Ala Glu Lys Arg	
	150 155 160 165	
10	aaa tct gat tat ata atc agg act cta aaa gtt aag ttc aat agt gaa	584
	Lys Ser Asp Tyr Ile Ile Arg Thr Leu Lys Val Lys Phe Asn Ser Glu	
	170 175 180	
	act cga act atc tac cag ttt cat tac aag aat tgg cca gac cat gat	632
	Thr Arg Thr Ile Tyr Gln Phe His Tyr Lys Asn Trp Pro Asp His Asp	
	185 190 195	
	gta cct tca tct ata gac cct att ctt gag ctc atc tgg gat gta cgt	680
	Val Pro Ser Ser Ile Asp Pro Ile Leu Glu Leu Ile Trp Asp Val Arg	
	200 205 210	
20	tgt tac caa gag gat gac agt gtt ccc ata tgc att cac tgc agt gct	728
	Cys Tyr Gln Glu Asp Asp Ser Val Pro Ile Cys Ile His Cys Ser Ala	
	215 220 225	
	ggc tgt gga agg act ggt gtt att tgt gct att gtt gat tat aca tgg	776
	Gly Cys Gly Arg Thr Gly Val Ile Cys Ala Ile Val Asp Tyr Thr Trp	
	230 235 240 245	
30	atg ttg cta aaa gat ggg ata att cct gag aac ttc agt gtt ttc agt	824
	Met Leu Leu Lys Asp Gly Ile Ile Pro Glu Asn Phe Ser Val Phe Ser	
	250 255 260	
	ttg atc cgg gaa atg cgg aca cag agg cct tca tta gtt caa acg cag	872
	Leu Ile Arg Glu Met Arg Thr Gln Arg Pro Ser Leu Val Gln Thr Gln	
	265 270 275	
	gaa caa tat gaa ctg gtc tac aat gct gta tta gaa cta ttt aag aga	920
	Glu Gln Tyr Glu Leu Val Tyr Asn Ala Val Leu Glu Leu Phe Lys Arg	
	280 285 290	
40	cag atg gat gtt atc aga gat aaa cat tct gga aca gag agt caa gca	968
	Gln Met Asp Val Ile Arg Asp Lys His Ser Gly Thr Glu Ser Gln Ala	
	295 300 305	
	aag cat tgt att cct gag aaa aat cac act ctc caa gca gac tct tat	1016
	Lys His Cys Ile Pro Glu Lys Asn His Thr Leu Gln Ala Asp Ser Tyr	
	310 315 320 325	
50	tct cct aat tta cca aaa agt acc aca aaa gca gca aaa atg atg aac	1064
	Ser Pro Asn Leu Pro Lys Ser Thr Thr Lys Ala Ala Lys Met Met Asn	
	330 335 340	
	caa caa agg aca aaa atg gaa atc aaa gaa tct tct tcc ttt gac ttt	1112
	Gln Gln Arg Thr Lys Met Glu Ile Lys Glu Ser Ser Ser Phe Asp Phe	
	345 350 355	

	agg	act	tct	gaa	ata	agt	gca	aaa	gaa	gag	cta	gtt	ttg	cac	cct	gct	1160
	Arg	Thr	Ser	Glu	Ile	Ser	Ala	Lys	Glu	Glu	Leu	Val	Leu	His	Pro	Ala	
			360					365					370				
	aaa	tca	agc	act	tct	ttt	gac	ttt	ctg	gag	cta	aat	tac	agt	ttt	gac	1208
	Lys	Ser	Ser	Thr	Ser	Phe	Asp	Phe	Leu	Glu	Leu	Asn	Tyr	Ser	Phe	Asp	
		375					380					385					
10	aaa	aat	gct	gac	aca	acc	atg	aaa	tgg	cag	aca	aag	gca	ttt	cca	ata	1256
	Lys	Asn	Ala	Asp	Thr	Thr	Met	Lys	Trp	Gln	Thr	Lys	Ala	Phe	Pro	Ile	
		390					395				400					405	
	gtt	ggg	gag	cct	ctt	cag	aag	cat	caa	agt	ttg	gat	ttg	ggc	tct	ctt	1304
	Val	Gly	Glu	Pro	Leu	Gln	Lys	His	Gln	Ser	Leu	Asp	Leu	Gly	Ser	Leu	
					410					415					420		
	ttg	ttt	gag	gga	tgt	tct	aat	tct	aaa	cct	gta	aat	gca	gca	gga	aga	1352
	Leu	Phe	Glu	Gly	Cys	Ser	Asn	Ser	Lys	Pro	Val	Asn	Ala	Ala	Gly	Arg	
				425					430					435			
20	tat	ttt	aat	tca	aag	gtg	cca	ata	aca	cgg	acc	aaa	tca	act	cct	ttt	1400
	Tyr	Phe	Asn	Ser	Lys	Val	Pro	Ile	Thr	Arg	Thr	Lys	Ser	Thr	Pro	Phe	
			440					445					450				
	gaa	ttg	ata	cag	cag	aga	gaa	acc	aag	gag	gtg	gac	agc	aag	gaa	aac	1448
	Glu	Leu	Ile	Gln	Gln	Arg	Glu	Thr	Lys	Glu	Val	Asp	Ser	Lys	Glu	Asn	
		455					460					465					
30	ttt	tct	tat	ttg	gaa	tct	caa	cca	cat	gat	tct	tgt	ttt	gta	gag	atg	1496
	Phe	Ser	Tyr	Leu	Glu	Ser	Gln	Pro	His	Asp	Ser	Cys	Phe	Val	Glu	Met	
		470				475				480						485	
	cag	gct	caa	aaa	gta	atg	cat	ggt	tct	tca	gca	gaa	ctg	aat	tat	tca	1544
	Gln	Ala	Gln	Lys	Val	Met	His	Val	Ser	Ser	Ala	Glu	Leu	Asn	Tyr	Ser	
					490				495						500		
	ctg	cca	tat	gac	tct	aaa	cac	caa	ata	cgt	aat	gcc	tct	aat	gta	aag	1592
	Leu	Pro	Tyr	Asp	Ser	Lys	His	Gln	Ile	Arg	Asn	Ala	Ser	Asn	Val	Lys	
				505				510					515				
40	cac	cat	gac	tct	agt	gct	ctt	ggt	gta	tat	tct	tac	ata	cct	tta	gtg	1640
	His	His	Asp	Ser	Ser	Ala	Leu	Gly	Val	Tyr	Ser	Tyr	Ile	Pro	Leu	Val	
			520					525					530				
	gaa	aat	cct	tat	ttt	tca	tca	tgg	cct	cca	agt	ggt	acc	agt	tct	aag	1688
	Glu	Asn	Pro	Tyr	Phe	Ser	Ser	Trp	Pro	Pro	Ser	Gly	Thr	Ser	Ser	Lys	
		535					540					545					
50	atg	tct	ctt	gat	tta	cct	gag	aag	caa	gat	gga	act	gtt	ttt	cct	tct	1736
	Met	Ser	Leu	Asp	Leu	Pro	Glu	Lys	Gln	Asp	Gly	Thr	Val	Phe	Pro	Ser	
		550				555					560					565	
	tct	ctg	ttg	cca	aca	tcc	tct	aca	tcc	ctc	ttc	tct	tat	tac	aat	tca	1784
	Ser	Leu	Leu	Pro	Thr	Ser	Ser	Thr	Ser	Leu	Phe	Ser	Tyr	Tyr	Asn	Ser	
					570					575					580		

cat agt tct tta tca ctg aat tct cca acc aat att tcc tca cta ttg 1832  
 His Ser Ser Leu Ser Leu Asn Ser Pro Thr Asn Ile Ser Ser Leu Leu  
 585 590 595

aac cag gag tca gct gta cta gca act gct cca agg ata gat gat gaa 1880  
 Asn Gln Glu Ser Ala Val Leu Ala Thr Ala Pro Arg Ile Asp Asp Glu  
 600 605 610

10 atc ccc cct cca ctt cct gta cgg aca cct gaa tca ttt att gtg gtt 1928  
 Ile Pro Pro Pro Leu Pro Val Arg Thr Pro Glu Ser Phe Ile Val Val  
 615 620 625

gag gaa gct gga gaa ttc tca cca aat gtt ccc aaa tcc tta tcc tca 1976  
 Glu Glu Ala Gly Glu Phe Ser Pro Asn Val Pro Lys Ser Leu Ser Ser  
 630 635 640 645

gct gtg aag gta aaa att gga aca tca ctg gaa tgg ggt gga aca tct 2024  
 Ala Val Lys Val Lys Ile Gly Thr Ser Leu Glu Trp Gly Gly Thr Ser  
 650 655 660

20 gaa cca aag aaa ttt gat gac tct gtg ata ctt aga cca agc aag agt 2072  
 Glu Pro Lys Lys Phe Asp Asp Ser Val Ile Leu Arg Pro Ser Lys Ser  
 665 670 675

gta aaa ctc cga agt cct aaa tca ggt aaa aat ttc tct tgg ctt 2117  
 Val Lys Leu Arg Ser Pro Lys Ser Gly Lys Asn Phe Ser Trp Leu  
 680 685 690

30 tagatgacat ttagccctaa gattggaaga atgggttcggt aagtttagag taattcactt 2177  
 caggaagtta cttggttccc ataatagctt ccagtattca ttgatttatt tctggctttc 2237  
 ccagactaga aattttgtaa agagtcattg gggaagctag ggctaaccag aaaataaaat 2297  
 aaaaataatg ggataaaaaa tcggaactac tgttttcccc ctagtcggag cacatccgg 2356

<210> 4  
 <211> 692  
 <212> PRT  
 <213> Homo sapiens

40 <400> 4  
 Met Asp Gln Arg Glu Ile Leu Gln Lys Phe Leu Asp Glu Ala Gln Ser  
 1 5 10 15  
 Lys Lys Ile Thr Lys Glu Glu Phe Ala Asn Glu Phe Leu Lys Leu Lys  
 20 25 30  
 Arg Gln Ser Thr Lys Tyr Lys Ala Asp Lys Thr Tyr Pro Thr Thr Val  
 35 40 45

50 Ala Glu Asn Ala Lys Asn Ile Lys Lys Asn Arg Tyr Lys Asp Ile Leu  
 50 55 60  
 Pro Tyr Asp Tyr Ser Arg Val Glu Leu Ser Leu Ile Thr Ser Asp Glu  
 65 70 75 80  
 Asp Ser Ser Tyr Ile Asn Ala Asn Phe Ile Lys Gly Val Tyr Gly Pro  
 85 90 95

	Lys	Ala	Tyr	Ile	Ala	Thr	Gln	Gly	Pro	Leu	Ser	Thr	Thr	Leu	Leu	Asp	
				100					105					110			
	Phe	Trp	Arg	Met	Ile	Trp	Glu	Tyr	Ser	Val	Leu	Ile	Ile	Val	Met	Ala	
			115					120					125				
	Cys	Met	Glu	Tyr	Glu	Met	Gly	Lys	Lys	Lys	Cys	Glu	Arg	Tyr	Trp	Ala	
		130					135					140					
10	Glu	Pro	Gly	Glu	Met	Gln	Leu	Glu	Phe	Gly	Pro	Phe	Ser	Val	Ser	Cys	
	145					150					155					160	
	Glu	Ala	Glu	Lys	Arg	Lys	Ser	Asp	Tyr	Ile	Ile	Arg	Thr	Leu	Lys	Val	
					165					170					175		
	Lys	Phe	Asn	Ser	Glu	Thr	Arg	Thr	Ile	Tyr	Gln	Phe	His	Tyr	Lys	Asn	
				180					185					190			
20	Trp	Pro	Asp	His	Asp	Val	Pro	Ser	Ser	Ile	Asp	Pro	Ile	Leu	Glu	Leu	
			195					200					205				
	Ile	Trp	Asp	Val	Arg	Cys	Tyr	Gln	Glu	Asp	Asp	Ser	Val	Pro	Ile	Cys	
		210					215					220					
	Ile	His	Cys	Ser	Ala	Gly	Cys	Gly	Arg	Thr	Gly	Val	Ile	Cys	Ala	Ile	
	225					230					235					240	
	Val	Asp	Tyr	Thr	Trp	Met	Leu	Leu	Lys	Asp	Gly	Ile	Ile	Pro	Glu	Asn	
					245					250					255		
30	Phe	Ser	Val	Phe	Ser	Leu	Ile	Arg	Glu	Met	Arg	Thr	Gln	Arg	Pro	Ser	
				260					265					270			
	Leu	Val	Gln	Thr	Gln	Glu	Gln	Tyr	Glu	Leu	Val	Tyr	Asn	Ala	Val	Leu	
			275					280					285				
	Glu	Leu	Phe	Lys	Arg	Gln	Met	Asp	Val	Ile	Arg	Asp	Lys	His	Ser	Gly	
		290					295					300					
40	Thr	Glu	Ser	Gln	Ala	Lys	His	Cys	Ile	Pro	Glu	Lys	Asn	His	Thr	Leu	
	305					310					315					320	
	Gln	Ala	Asp	Ser	Tyr	Ser	Pro	Asn	Leu	Pro	Lys	Ser	Thr	Thr	Lys	Ala	
					325					330					335		
	Ala	Lys	Met	Met	Asn	Gln	Gln	Arg	Thr	Lys	Met	Glu	Ile	Lys	Glu	Ser	
				340					345					350			
50	Ser	Ser	Phe	Asp	Phe	Arg	Thr	Ser	Glu	Ile	Ser	Ala	Lys	Glu	Glu	Leu	
			355					360					365				
	Val	Leu	His	Pro	Ala	Lys	Ser	Ser	Thr	Ser	Phe	Asp	Phe	Leu	Glu	Leu	
		370					375					380					
	Asn	Tyr	Ser	Phe	Asp	Lys	Asn	Ala	Asp	Thr	Thr	Met	Lys	Trp	Gln	Thr	
	385					390					395					400	

[illegible]

<210> 5  
 <211> 802  
 <212> PRT  
 <213> Mus musculus

<400> 5

	Met	Asp	Gln	Arg	Glu	Ile	Leu	Gln	Gln	Leu	Leu	Lys	Glu	Ala	Gln	Lys
	1				5					10					15	
10	Lys	Lys	Leu	Asn	Ser	Glu	Glu	Phe	Ala	Ser	Glu	Phe	Leu	Lys	Leu	Lys
				20					25					30		
	Arg	Gln	Ser	Thr	Lys	Tyr	Lys	Ala	Asp	Lys	Ile	Tyr	Pro	Thr	Thr	Val
			35					40					45			
	Ala	Gln	Arg	Pro	Lys	Asn	Ile	Lys	Lys	Asn	Arg	Tyr	Lys	Asp	Ile	Leu
	50					55						60				
20	Pro	Tyr	Asp	His	Ser	Leu	Val	Glu	Leu	Ser	Leu	Leu	Thr	Ser	Asp	Glu
	65					70					75				80	
	Asp	Ser	Ser	Tyr	Ile	Asn	Ala	Ser	Phe	Ile	Lys	Gly	Val	Tyr	Gly	Pro
					85					90					95	
	Lys	Ala	Tyr	Ile	Ala	Thr	Gln	Gly	Pro	Leu	Ser	Thr	Thr	Leu	Leu	Asp
				100					105					110		
	Phe	Trp	Arg	Met	Ile	Trp	Glu	Tyr	Arg	Ile	Leu	Val	Ile	Val	Met	Ala
			115					120						125		
30	Cys	Met	Glu	Phe	Glu	Met	Gly	Lys	Lys	Lys	Cys	Glu	Arg	Tyr	Trp	Ala
	130						135					140				
	Glu	Pro	Gly	Glu	Thr	Gln	Leu	Gln	Phe	Gly	Pro	Phe	Ser	Ile	Ser	Cys
	145					150					155				160	
	Glu	Ala	Glu	Lys	Lys	Lys	Ser	Asp	Tyr	Lys	Ile	Arg	Thr	Leu	Lys	Ala
				165						170					175	
40	Lys	Phe	Asn	Asn	Glu	Thr	Arg	Ile	Ile	Tyr	Gln	Phe	His	Tyr	Lys	Asn
				180					185					190		
	Trp	Pro	Asp	His	Asp	Val	Pro	Ser	Ser	Ile	Asp	Pro	Ile	Leu	Gln	Leu
			195					200					205			
	Ile	Trp	Asp	Met	Arg	Cys	Tyr	Gln	Glu	Asp	Asp	Cys	Val	Pro	Ile	Cys
	210						215					220				
	Ile	His	Cys	Ser	Ala	Gly	Cys	Gly	Arg	Thr	Gly	Val	Ile	Cys	Ala	Val
50	225					230					235				240	
	Asp	Tyr	Thr	Trp	Met	Leu	Leu	Lys	Asp	Gly	Ile	Ile	Pro	Lys	Asn	Phe
				245						250					255	
	Ser	Val	Phe	Asn	Leu	Ile	Gln	Glu	Met	Arg	Thr	Gln	Arg	Pro	Ser	Leu
				260					265					270		

	Val	Gln	Thr	Gln	Glu	Gln	Tyr	Glu	Leu	Val	Tyr	Ser	Ala	Val	Leu	Glu	
					275			280					285				
	Leu	Phe	Lys	Arg	His	Met	Asp	Val	Ile	Ser	Asp	Asn	His	Leu	Gly	Arg	
		290					295					300					
	Glu	Ile	Gln	Ala	Gln	Cys	Ser	Ile	Pro	Glu	Gln	Ser	Leu	Thr	Val	Glu	
	305					310					315					320	
10	Ala	Asp	Ser	Cys	Pro	Leu	Asp	Leu	Pro	Lys	Asn	Ala	Met	Arg	Asp	Val	
					325					330					335		
	Lys	Thr	Thr	Asn	Gln	His	Ser	Lys	Gln	Gly	Ala	Glu	Ala	Glu	Ser	Thr	
				340					345					350			
	Gly	Gly	Ser	Ser	Leu	Gly	Leu	Arg	Thr	Ser	Thr	Met	Asn	Ala	Glu	Glu	
			355					360					365				
20	Glu	Leu	Val	Leu	His	Ser	Ala	Lys	Ser	Ser	Pro	Ser	Phe	Asn	Cys	Leu	
		370					375					380					
	Glu	Leu	Asn	Cys	Gly	Cys	Asn	Asn	Lys	Ala	Val	Ile	Thr	Arg	Asn	Gly	
	385					390					395					400	
	Gln	Ala	Arg	Ala	Ser	Pro	Val	Val	Gly	Glu	Pro	Leu	Gln	Lys	Tyr	Gln	
					405					410					415		
	Ser	Leu	Asp	Phe	Gly	Ser	Met	Leu	Phe	Gly	Ser	Cys	Pro	Ser	Ala	Leu	
				420					425					430			
30	Pro	Ile	Asn	Thr	Ala	Asp	Arg	Tyr	His	Asn	Ser	Lys	Gly	Pro	Val	Lys	
			435					440					445				
	Arg	Thr	Lys	Ser	Thr	Pro	Phe	Glu	Leu	Ile	Gln	Gln	Arg	Lys	Thr	Asn	
		450					455					460					
	Asp	Leu	Ala	Val	Gly	Asp	Gly	Phe	Ser	Cys	Leu	Glu	Ser	Gln	Leu	His	
	465					470					475					480	
40	Glu	His	Tyr	Ser	Leu	Arg	Glu	Leu	Gln	Val	Gln	Arg	Val	Ala	His	Val	
					485				490						495		
	Ser	Ser	Glu	Glu	Leu	Asn	Tyr	Ser	Leu	Pro	Gly	Ala	Cys	Asp	Ala	Ser	
				500					505					510			
	Cys	Val	Pro	Arg	His	Ser	Pro	Gly	Ala	Leu	Arg	Val	His	Leu	Tyr	Thr	
			515					520					525				
50	Ser	Leu	Ala	Glu	Asp	Pro	Tyr	Phe	Ser	Ser	Ser	Pro	Pro	Asn	Ser	Ala	
		530					535					540					
	Asp	Ser	Lys	Met	Ser	Phe	Asp	Leu	Pro	Glu	Lys	Gln	Asp	Gly	Ala	Thr	
	545					550					555					560	
	Ser	Pro	Gly	Ala	Leu	Leu	Pro	Ala	Ser	Ser	Thr	Thr	Ser	Phe	Phe	Tyr	
					565					570					575		

Ser Asn Pro His Asp Ser Leu Val Met Asn Thr Leu Thr Ser Phe Ser  
 580 585 590  
 Pro Pro Leu Asn Gln Glu Thr Ala Val Glu Ala Pro Ser Arg Arg Thr  
 595 600 605  
 Asp Asp Glu Ile Pro Pro Pro Leu Pro Glu Arg Thr Pro Glu Ser Phe  
 610 615 620  
 10 Ile Val Val Glu Glu Ala Gly Glu Pro Ser Pro Arg Val Thr Glu Ser  
 625 630 635 640  
 Leu Pro Leu Val Val Thr Phe Gly Ala Ser Pro Glu Cys Ser Gly Thr  
 645 650 655  
 Ser Glu Met Lys Ser His Asp Ser Val Gly Phe Thr Pro Ser Lys Asn  
 660 665 670  
 20 Val Lys Leu Arg Ser Pro Lys Ser Asp Arg His Gln Asp Gly Ser Pro  
 675 680 685  
 Pro Pro Pro Leu Pro Glu Arg Thr Leu Glu Ser Phe Phe Leu Ala Asp  
 690 695 700  
 Glu Asp Cys Ile Gln Ala Gln Ala Val Gln Thr Ser Ser Thr Ser Tyr  
 705 710 715 720  
 Pro Glu Thr Thr Glu Asn Ser Thr Ser Ser Lys Gln Thr Leu Arg Thr  
 725 730 735  
 30 Pro Gly Lys Ser Phe Thr Arg Ser Lys Ser Leu Lys Ile Phe Arg Asn  
 740 745 750  
 Met Lys Lys Ser Val Cys Asn Ser Ser Ser Pro Ser Lys Pro Thr Glu  
 755 760 765  
 Arg Val Gln Pro Lys Asn Ser Ser Ser Phe Leu Asn Phe Gly Phe Gly  
 770 775 780  
 40 Asn Arg Phe Ser Lys Pro Lys Gly Pro Arg Asn Pro Pro Ser Ala Trp  
 785 790 795 800

Asn Met

<210> 6  
 <211> 82  
 <212> DNA  
 <213> Homo sapiens

50

<400> 6  
 aaactccgaa gtcctaaatc aggtaaaaat ttctcttggc tttagatgac atttagccct 60  
 aagattggaa gaatggttcg tt 82

<210> 7  
 <211> 14



17/17

<212> PRT

<213> Homo sapiens

<400> 7

Lys	Leu	Arg	Ser	Pro	Lys	Ser	Gly	Lys	Asn	Phe	Ser	Trp	Leu
1				5					10				